SEQUENCE LISTING

<110> Finlay, Brett B.
Kenny, Brendant
DeVinney, Rebekah
Stein, Marcus

<120> HOST RECEPTOR FOR PATHOGENIC BACTERIA

<130> UBCV-0004

<140> US 09/189,415
<141> 1998-11-10

<150> US 60/065,130
<151> 1997-11-12

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<170> PatentIn version 3.3

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aaaggggggc ttgatactct taactctgct attggatctt cgttattccg tgttgaaact 180

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gtatttactg gaggccgcgg tggcccaggg catgctatgg tcacggttgc ttcagatatc 360

gccgaagccc gtcagaggat aatagataaa ttagaaccaa aggatacaaa ggagacgaag 420

gagccagggg atccaaatag tggcgaggga aaaatcattg aaattcatac ctcaacctca 480

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<213> Escherichia coli

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Gly Thr Gly His Leu Ile Ser Ser Thr Gly Ala Leu Gly Ser Arg Ser
        35                  40                  45

Leu Phe Ser Pro Leu Arg Asn Ser Met Ala Asp Ser Val Asp Ser Arg
    50                  55                  60

Asp Ile Pro Gly Leu Pro Thr Asn Pro Ser Arg Leu Ala Ala Ala Thr
65                  70                  75                  80

Ser Glu Thr Cys Leu Leu Gly Gly Phe Glu Val Leu His Asp Lys Gly
                85                  90                  95

Pro Leu Asp Ile Leu Asn Thr Gln Ile Gly Pro Ser Ala Phe Arg Val
            100                 105                 110

Glu Val Gln Ala Asp Gly Thr His Ala Ala Ile Gly Glu Lys Asn Gly
        115                 120                 125

Leu Glu Val Ser Val Thr Leu Ser Pro Gln Glu Trp Ser Ser Leu Gln
    130                 135                 140

Ser Ile Asp Thr Glu Gly Lys Asn Arg Phe Val Phe Thr Gly Gly Arg
145                 150                 155                 160

Gly Gly Ser Gly His Pro Met Val Thr Val Ala Ser Asp Ile Ala Glu
                165                 170                 175

Ala Arg Thr Lys Ile Leu Ala Lys Leu Asp Pro Asp Asn His Gly Gly
            180                 185                 190

Arg Gln Pro Lys Asp Val Asp Thr Arg Ser Val Gly Val Gly Ser Ala
        195                 200                 205

Ser Gly Ile Asp Asp Gly Val Val Ser Glu Thr His Thr Ser Thr Thr
    210                 215                 220

Asn Ser Ser Val Arg Ser Asp Pro Lys Phe Trp Val Ser Val Gly Ala
225                 230                 235                 240

Ile Ala Ala Gly Leu Ala Gly Leu Ala Ala Thr Gly Ile Ala Gln Ala
                245                 250                 255

Leu Ala Leu Thr Pro Glu Pro Asp Asp Pro Thr Thr Thr Asp Pro Asp
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260 265 270

Gln Ala Ala Asn Ala Ala Glu Ser Ala Thr Lys Asp Gln Leu Thr Gln
275 280 285

Glu Ala Phe Lys Asn Pro Glu Asn Gln Lys Val Asn Ile Asp Ala Asn
290 295 300

Gly Asn Ala Ile Pro Ser Gly Glu Leu Lys Asp Asp Ile Val Glu Gln
305 310 315 320

Ile Ala Gln Gln Ala Lys Glu Ala Gly Glu Val Ala Arg Gln Gln Ala
325 330 335

Val Glu Ser Asn Ala Gln Ala Gln Gln Arg Tyr Glu Asp Gln His Ala
340 345 350

Arg Arg Gln Glu Glu Leu Gln Leu Ser Ser Gly Ile Gly Tyr Gly Leu
355 360 365

Ser Ser Ala Leu Ile Val Ala Gly Gly Ile Gly Ala Gly Val Thr Thr
370 375 380

Ala Leu His Arg Arg Asn Gln Pro Ala Glu Gln Thr Thr Thr Thr Thr
385 390 395 400

Thr His Thr Val Val Gln Gln Gln Thr Gly Gly Ile Pro Gln His Lys
405 410 415

Val Ala Leu Met Pro Gln Glu Arg Arg Arg Phe Ser Asp Arg Arg Asp
420 425 430

Ser Gln Gly Ser Val Ala Ser Thr His Trp Ser Asp Ser Ser Ser Glu
435 440 445

Val Val Asn Pro Tyr Ala Glu Val Gly Gly Ala Arg Asn Ser Leu Ser
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Ala His Gln Pro Glu Glu His Ile Tyr Asp Glu Val Ala Ala Asp Pro
465 470 475 480

Gly Tyr Ser Val Ile Gln Asn Phe Ser Gly Ser Gly Pro Val Thr Gly
485 490 495

Arg Leu Ile Gly Thr Pro Gly Gln Gly Ile Gln Ser Thr Tyr Ala Leu
500 505 510

Leu Ala Asn Ser Gly Gly Leu Arg Leu Gly Met Gly Gly Leu Thr Ser
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Gly Gln Leu Ile Asn Ser Thr Gly Pro Leu Gly Ser Arg Ala Leu Phe
35 40 45

Thr Pro Val Arg Asn Ser Met Ala Asp Ser Gly Asp Asn Arg Ala Ser
50 55 60

Asp Val Pro Gly Leu Pro Val Asn Pro Met Arg Leu Ala Ala Ser Glu
65 70 75 80

Ile Thr Leu Asn Asp Gly Phe Glu Val Leu His Asp His Gly Pro Leu
85 90 95

Asp Thr Leu Asn Arg Gln Ile Gly Ser Ser Val Phe Arg Val Glu Thr
100 105 110

Gln Glu Asp Gly Lys His Ile Ala Val Gly Gln Arg Asn Gly Val Glu
115 120 125

Thr Ser Val Val Leu Ser Asp Gln Glu Tyr Ala Arg Leu Gln Ser Ile
130 135 140

Asp Pro Glu Gly Lys Asp Lys Phe Val Phe Thr Gly Gly Arg Gly Gly
145 150 155 160

Ala Gly His Ala Met Val Thr Val Ala Ser Asp Ile Thr Glu Ala Arg
165 170 175

Gln Arg Ile Leu Glu Leu Leu Glu Pro Lys Gly Thr Gly Glu Ser Lys
180 185 190

Gly Ala Gly Glu Ser Lys Gly Val Gly Glu Leu Arg Glu Ser Asn Ser
195 200 205

Gly Ala Glu Asn Thr Thr Glu Thr Gln Thr Ser Thr Ser Thr Ser Ser
210 215 220

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Gly Leu Ile Gly Leu Ala Ala Thr Gly Ile Val Gln Ala Leu Ala Leu
                245                 250                 255

Thr Pro Glu Pro Asp Ser Pro Thr Thr Thr Asp Pro Asp Ala Ala Ala
            260                 265                 270

Ser Ala Thr Glu Thr Ala Thr Arg Asp Gln Leu Thr Lys Glu Ala Phe
        275                 280                 285

Gln Asn Pro Asp Asn Gln Lys Val Asn Ile Asp Glu Leu Gly Asn Ala
    290                 295                 300

Ile Pro Ser Gly Val Leu Lys Asp Asp Val Val Ala Asn Ile Glu Glu
305                 310                 315                 320

Gln Ala Lys Ala Ala Gly Glu Glu Ala Lys Gln Gln Ala Ile Glu Asn
                325                 330                 335

Asn Ala Gln Ala Gln Lys Lys Tyr Asp Glu Gln Gln Ala Lys Arg Gln
            340                 345                 350

Glu Glu Leu Lys Val Ser Ser Gly Ala Gly Tyr Gly Leu Ser Gly Ala
        355                 360                 365

Leu Ile Leu Gly Gly Gly Ile Gly Val Ala Val Thr Ala Ala Leu His
    370                 375                 380

Arg Lys Asn Gln Pro Val Glu Gln Thr Thr Thr Thr Thr Thr Thr Thr
385                 390                 395                 400

Thr Thr Thr Ser Ala Arg Thr Val Glu Asn Lys Pro Ala Asn Asn Thr
                405                 410                 415

Pro Ala Gln Gly Asn Val Asp Thr Pro Gly Ser Glu Asp Thr Met Glu
            420                 425                 430

Ser Arg Arg Ser Ser Met Ala Ser Thr Ser Ser Thr Phe Phe Asp Thr
        435                 440                 445

Ser Ser Ile Gly Thr Val Gln Asn Pro Tyr Ala Asp Val Lys Thr Ser
    450                 455                 460

Leu His Asp Ser Gln Val Pro Thr Ser Asn Ser Asn Thr Ser Val Gln
465                 470                 475                 480

Asn Met Gly Asn Thr Asp Ser Val Val Tyr Ser Thr Ile Gln His Pro
                485                 490                 495
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Pro Arg Asp Thr Thr Asp Asn Gly Ala Arg Leu Leu Gly Asn Pro Ser
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Ala Gly Ile Gln Ser Thr Tyr Ala Arg Leu Ala Leu Ser Gly Gly Leu
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530 535 540

Thr Ser Asn Asn Pro Pro Ala Pro Gly Ser His Arg Phe Val
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35 40 45

Ser Ala Ile Gly Ser Ser Leu Phe Arg Val Glu Thr Arg Asp Asp Gly
50 55 60

Ser His Val Ala Ile Gly Gln Lys Asn Gly Leu Glu Thr Thr Val Val
65 70 75 80

Leu Ser Glu Gln Glu Phe Ser Ser Leu Gln Ser Leu Asp Pro Glu Gly
85 90 95

Lys Asn Lys Phe Val Phe Thr Gly Gly Arg Gly Gly Pro Gly His Ala
100 105 110

Met Val Thr Val Ala Ser Asp Ile Ala Glu Ala Arg Gln Arg Ile Ile
115 120 125

Asp Lys Leu Glu Pro Lys Asp Thr Lys Glu Thr Lys Glu Pro Gly Asp
130 135 140

Pro Asn Ser Gly Glu Gly Lys Ile Ile Glu Ile His Thr Ser Thr Ser
145 150 155 160

Thr Ser Ser Leu Arg Ala Asp Pro Lys Leu Trp Leu Ser Leu Gly Thr
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Ile Ala Ala Gly Leu Ile Gly Met Ala Ala Thr Gly Ile Ala Gln Ala
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Val Ala Leu Thr Pro Glu Pro Asp Asp Pro Ile Thr Thr Asp Pro Asp
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Ala Ala Ala Asn Thr Ala Glu Ala Ala Ala Lys Asp Gln Leu Thr Lys
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Glu Ala Phe Gln Asn Pro Asp Asn Gln Lys Val Asn Ile Asp Glu Asn
225                 230                 235                 240

Gly Asn Ala Ile Pro Ser Gly Glu Leu Lys Asp Asp Val Val Ala Gln
                245                 250                 255

Ile Ala Glu Gln Ala Lys Ala Ala Gly Glu Gln Ala Arg Gln Glu Ala
            260                 265                 270

Ile Glu Ser Asn Ser Gln Ala Gln Gln Lys Tyr Asp Glu Gln His Ala
        275                 280                 285

Lys Arg Glu Gln Glu Met Ser Leu Ser Ser Gly Val Gly Tyr Gly Ile
    290                 295                 300

Ser Gly Ala Leu Ile Leu Gly Gly Gly Ile Gly Ala Gly Val Thr Ala
305                 310                 315                 320

Ala Leu His Arg Lys Asn Gln Pro Ala Glu Gln Thr Ile Thr Thr Arg
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Thr Val Val Asp Asn Gln Pro Thr Asn Asn Ala Ser Ala Gln Gly Asn
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Thr Asp Thr Ser Gly Pro Glu Glu Ser Pro Ala Ser Arg Arg Asn Ser
        355                 360                 365

Asn Ala Ser Leu Ala Ser Asn Gly Ser Asp Thr Ser Ser Thr Gly Thr
    370                 375                 380

Val Glu Asn Pro Tyr Ala Asp Val Gly Met Pro Arg Asn Asp Ser Leu
385                 390                 395                 400

Ala Arg Ile Ser Glu Glu Pro Ile Tyr Asp Glu Val Ala Ala Asp Pro
                405                 410                 415

Asn Tyr Ser Val Ile Gln His Phe Ser Gly Asn Ser Pro Val Thr Gly
            420                 425                 430

Arg Leu Val Gly Thr Pro Gly Gln Gly Ile Gln Ser Thr Tyr Ala Leu
        435                 440                 445
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<212> PRT
<213> Escherichia coli

<400> 14

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35 40 45

Leu Phe Ser Pro Leu Arg Asn Ser Met Ala Asp Ser Val Asp Ser Arg
50 55 60

Asp Ile Pro Gly Leu Pro Thr Asn Pro Ser Arg Leu Ala Ala Ala Thr
65 70 75 80

Ser Glu Thr Cys Leu Leu Gly Gly Phe Glu Val Leu His Asp Lys Gly
85 90 95

Pro Leu Asp Ile Leu Asn Thr Gln Ile Gly Pro Ser Ala Phe Arg Val
100 105 110

Glu Val Gln Ala Asp Gly Thr His Ala Ala Ile Gly Glu Lys Asn Gly
115 120 125

Leu Glu Val Ser Val Thr Leu Ser Pro Gln Glu Trp Ser Ser Leu Gln
130 135 140

Ser Ile Asp Thr Glu Gly Lys Asn Arg Phe Val Phe Thr Gly Gly Arg
145 150 155 160

Gly Gly Ser Gly His Pro Met Val Thr Val Ala Ser Asp Ile Ala Glu
165 170 175

Ala Arg Thr Lys Ile Leu Ala Lys Leu Asp Pro Asp Asn His Gly Gly

180 185 190

Arg Gln Pro Lys Asp Val Asp Thr Arg Ser Val Gly Val Gly Ser Ala
195 200 205

Ser Gly Ile Asp Asp Gly Val Val Ser Glu Thr His Thr Ser Thr Thr
210 215 220

Asn Ser Ser Val Arg Ser Asp Pro Lys Phe Trp Val Ser Val Gly Ala
225 230 235 240

Ile Ala Ala Gly Leu Ala Gly Leu Ala Ala Thr Gly Ile Ala Gln Ala
245 250 255

Leu Ala Leu Thr Pro Glu Pro Asp Asp Pro Thr Thr Thr Asp Pro Asp
260 265 270

Gln Ala Ala Asn Ala Ala Glu Ser Ala Thr Lys Asp Gln Leu Thr Gln
275 280 285

Glu Ala Phe Lys Asn Pro Glu Asn Gln Lys Val Asn Ile Asp Ala Asn
290 295 300

Gly Asn Ala Ile Pro Ser Gly Glu Leu Lys Asp Asp Ile Val Glu Gln
305 310 315 320

Ile Ala Gln Gln Ala Lys Glu Ala Gly Glu Val Ala Arg Gln Gln Ala
325 330 335

Val Glu Ser Asn Ala Gln Ala Gln Gln Arg Tyr Glu Asp Gln His Ala
340 345 350

Arg Arg Gln Glu Glu Leu Gln Leu Ser Ser Gly Ile Gly Tyr Gly Leu
355 360 365

Ser Ser Ala Leu Ile Val Ala Gly Gly Ile Gly Ala Gly Val Thr Thr
370 375 380

Ala Leu His Arg Arg Asn Gln Pro Ala Glu Gln Thr Thr Thr Thr Thr
385 390 395 400

Thr His Thr Val Val Gln Gln Gln Thr Gly Gly Ile Pro Gln His Lys
405 410 415

Val Ala Leu Met Pro Gln Glu Arg Arg Arg Phe Ser Asp Arg Arg Asp
420 425 430

Ser Gln Gly Ser Val Ala Ser Thr His Trp Ser Asp Ser Ser Ser Glu
435 440 445

Val Val Asn Pro Tyr Ala Glu Val Gly Gly Ala Arg Asn Ser Leu Ser

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    450                 455                 460

Ala His Gln Pro Glu Glu His Ile Tyr Asp Glu Val Ala Ala Asp Pro
465                 470                 475                 480

Gly Tyr Ser Val Ile Gln Asn Phe Ser Gly Ser Gly Pro Val Thr Gly
                485                 490                 495

Arg Leu Ile Gly Thr Pro Gly Gln Gly Ile Gln Ser Thr Tyr Ala Leu
            500                 505                 510

Leu Ala Asn Ser Gly Gly Leu Arg Leu Gly Met Gly Gly Leu Thr Ser
        515                 520                 525

Gly Gly Glu Thr Ala Val Ser Ser Val Asn Ala Ala Pro Thr Pro Gly
    530                 535                 540

Pro Val Arg Phe Val Met Ser Ser Arg Ser Glu Leu Leu Leu Asp Arg
545                 550                 555                 560

Phe Ala Glu Lys Ile Gly Val Gly Ser Ile Ser
                565                 570
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